

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/445,223A  
Source: 1FW16  
Date Processed by STIC: 5/6/05

***ENTERED***



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/445,223A

DATE: 05/06/2005

TIME: 15:22:14

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\05062005\I445223A.raw

3 <110> APPLICANT: WALLACH, David  
 4 BOLDIN, Mark  
 5 MALININ, Nikolai  
 7 <120> TITLE OF INVENTION: MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND

CELL

8 SURVIVAL PATHWAYS

10 <130> FILE REFERENCE: WALLACH=24  
 12 <140> CURRENT APPLICATION NUMBER: 09/445,223A  
 13 <141> CURRENT FILING DATE: 1999-12-06  
 15 <150> PRIOR APPLICATION NUMBER: IL 121011  
 16 <151> PRIOR FILING DATE: 1997-06-05  
 18 <150> PRIOR APPLICATION NUMBER: IL 121199  
 19 <151> PRIOR FILING DATE: 1997-06-30  
 21 <150> PRIOR APPLICATION NUMBER: IL 121746  
 22 <151> PRIOR FILING DATE: 1997-09-11  
 24 <160> NUMBER OF SEQ ID NOS: 3  
 26 <170> SOFTWARE: PatentIn version 3.3  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 540  
 30 <212> TYPE: PRT

31 &lt;213&gt; ORGANISM: Homo sapiens

33 &lt;400&gt; SEQUENCE: 1

35 Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His  
 36 1 5 10 15  
 39 Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val  
 40 20 25 30  
 43 Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His  
 44 35 40 45  
 47 Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu  
 48 50 55 60  
 51 Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Phe Pro  
 52 65 70 75 80  
 55 Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu  
 56 85 90 95  
 59 Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu  
 60 100 105 110  
 63 Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile  
 64 115 120 125  
 67 Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His  
 68 130 135 140  
 71 His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val  
 72 145 150 155 160  
 75 Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser  
 76 165 170 175

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79 Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr  
80 180 185 190  
83 Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile  
84 195 200 205  
87 Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser  
88 210 215 220  
91 Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr  
92 225 230 235 240  
95 Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro  
96 245 250 255  
99 Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly  
100 260 265 270  
103 Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile  
104 275 280 285  
107 Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu  
108 290 295 300  
111 Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala  
112 305 310 315 320  
115 Ile His Leu Cys Asp Lys Lys Met Glu Leu Ser Leu Asn Ile Pro  
116 325 330 335  
119 Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His  
120 340 345 350  
123 Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln  
124 355 360 365  
127 Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys  
128 370 375 380  
131 Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly  
132 385 390 395 400  
135 Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser  
136 405 410 415  
139 Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln  
140 420 425 430  
143 Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val  
144 435 440 445  
147 Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu  
148 450 455 460  
151 Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys  
152 465 470 475 480  
155 Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile  
156 485 490 495  
159 Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn  
160 500 505 510  
163 Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg  
164 515 520 525  
167 Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met  
168 530 535 540  
171 <210> SEQ ID NO: 2  
172 <211> LENGTH: 2098  
173 <212> TYPE: DNA

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174 <213> ORGANISM: Homo sapiens  
 176 <400> SEQUENCE: 2  
 177 ggccattatg gatggatggg cggcgctacg gcgttggcac cagtctctag aaaaagaagtc 60  
 179 agctctgggtt cggagaagca gcggcgtggcg tggggcatcc ggggaatggg cgcctcg 120  
 181 acctagtgtt gcggggcaaa aagggtcttg ccggcctcg ctcgtgcaggg gcgtatctgg 180  
 183 gcgcctgagc gcggcggtggg agccttggga gccgcgcgcag cagggggcac acccgaaacc 240  
 185 ggctcgagcg cccgggacca tgaacgggga ggccatctgc agcgccctgc ccaccattcc 300  
 187 ctaccacaaa ctcgccgacc tgcgtcacct gagccgcgcgc gcctctggca ctgtgtcg 360  
 189 cgcccgccac gcagactggc gcgtccaggt ggccgtgaag cacctgcaca tccacactcc 420  
 191 gctgctcgac agtgaagaa agatgtttt aagagaagct gaaattttac acaaagctag 480  
 193 atttagttac attttccaa ttttgggaat ttgaatgag cctgaattt tggaaatagt 540  
 195 tactgaatac atgccaaatg gatcattaaa tgaactccta cataggaaaa ctgaatatcc 600  
 197 ttagttgc tggccattga gatttcgcatt cctgcatttga attggcccttgcgtt 660  
 199 cctgcacaat atgactcctc ctttacttca tcatgacttg aagactcaga atatcttatt 720  
 201 ggacaatgaa tttcatgttta agattgcaga ttttggttta tcaaagtggc gcatgtatgtc 780  
 203 cctctcacag tcacgaagta gcaaattctgc accagaagga gggacaatta tttatatgccc 840  
 205 acctgaaaac tatgaacctg gacaaaaatc aaggccagt atcaagcactg atatataatag 900  
 207 ctatgcagtt atcacatggg aagtgttatac cagaaaaacag cctttgaag atgtcacc 960  
 209 tccttgcag ataatgtata gtgtgtcaca aggacatcga cctgttattat atgaagaaag 1020  
 211 tttgccccat gatataccctc accgagcacg tatgtatctc ctaatagaaa gtggatggc 1080  
 213 acaaaaatcca gatgaaagac catctttttt aaaaatgttta atagaacttgc aaccagg 1140  
 215 gagaacattt gaagagataa cttttcttga agctgttattt cagctaaaga aaacaaagtt 1200  
 217 acagagtgtt tcaagtgcca ttcacctatg tgacaagaag aaaaatggaaat tatctctgaa 1260  
 219 catacctgtt aatcatggc cacaagagga atcatgttgc tccctctcagc tccatgaaaa 1320  
 221 tagtggttct cctgaaactt caaggtccctt gccagctcctt caagacaatg atttttatac 1380  
 223 tagaaaaagctt caagactgtt attttatgaa gctgcattcac tgcattgttgcatttgc 1440  
 225 gatagcacc atttctggat ctcaaaggc tgcattctgtt gatcacaaga ccactccatg 1500  
 227 ctcttcagca ataataaattt cactctcaac tgcaggaaac tcagaacgtc tgcagccctgg 1560  
 229 tatagcccaag cagtggatcc agagaaaaag ggaagacattt gtaacc 1620  
 231 ctgccttaac cagtcgttag atgccttgc tgcaggac ttgtatcatgaa aagaggacta 1680  
 233 tgaacttgcgtt agtaccaagc ctacaaggac ctcaaaagtc agacaatttac tagacactac 1740  
 235 tgacatccaa ggagaagaat ttgccaaatgt tatagttacaa aatttggaaat ataaacaaaca 1800  
 237 aatgggttctt cagccttacc cggaaataact tgcgttttttgcgttgcatttgcatttgc 1860  
 239 acttcaaaat aaaagcatgt aagtgtactgtt tttcaagaa gaaaatgtttt tcataaaaagg 1920  
 241 atattttat ctctttgcgtt tgcattttt ttatataaaa tccgtgatgtt taaagcttw 1980  
 243 awraargkt cttsrktaa atattgtctt ccctccatgtt cactgcgttgcatttgcatttgc 2040  
 245 ttaatacacaag taaaaagttt aatttggaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 2098  
 248 <210> SEQ ID NO: 3  
 249 <211> LENGTH: 4  
 250 <212> TYPE: PRT  
 251 <213> ORGANISM: Artificial  
 253 <220> FEATURE:  
 254 <223> OTHER INFORMATION: Synthetic  
 257 <220> FEATURE:  
 258 <221> NAME/KEY: misc\_feature  
 259 <222> LOCATION: (1)..(1)  
 260 <223> OTHER INFORMATION: Residue at position 1 is modified by an acetyl group.  
 262 <220> FEATURE:  
 263 <221> NAME/KEY: misc\_feature

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Input Set : A:\sequence listing.txt  
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264 <222> LOCATION: (4)..(4)  
265 <223> OTHER INFORMATION: Residue at position 4 is modified by  
266 a-(4-methyl-coumaryl-7-amide).  
268 <220> FEATURE:  
269 <221> NAME/KEY: misc\_feature  
270 <222> LOCATION: (4)..(4)  
271 <223> OTHER INFORMATION: Residue at position 4 is modified by an AC-DEVD-AMC group.  
273 <400> SEQUENCE: 3  
275 Asp Glu Val Asp  
276 1

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/06/2005  
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Input Set : A:\sequence\_listing.txt  
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### Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq# : 3

**VERIFICATION SUMMARY**

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